

09831050 "11301

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181	acacaatagg	gaaatggaga	aaatgtactc	tgaacacccat	gaaaagggaa	cctgaaaatc
241	taatgtgtaa	acttggagaa	atgacattag	aaaacgaaag	ctacaaaaga	gaacactctt
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841	aaggatccat	gattacctgg	aaaaccagga	ctacagcacc	tgtgcctggg	ccattgtcca
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1141	tgcattattga	ccacaattgt	ttttattttg	taatgtggct	ttatatatto	tatccatttt
1201	a					

Figure 1

MIKHFFGTVLVLLASTTIFSLDLKLIIFQQRQVNQESLKLLNKLQTL~~SIQQ~~CLPH  
RKNFLLPQKSLSPQQYQKGHTLAILHEMLQQIFSLFRANISLDGWEENHTEK  
FLIQLHQQLEYLEALMGLEAEKLSGTLGSDNRLQVKMYFRRIHDYLENQD  
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Figure 2

09381050-11301  
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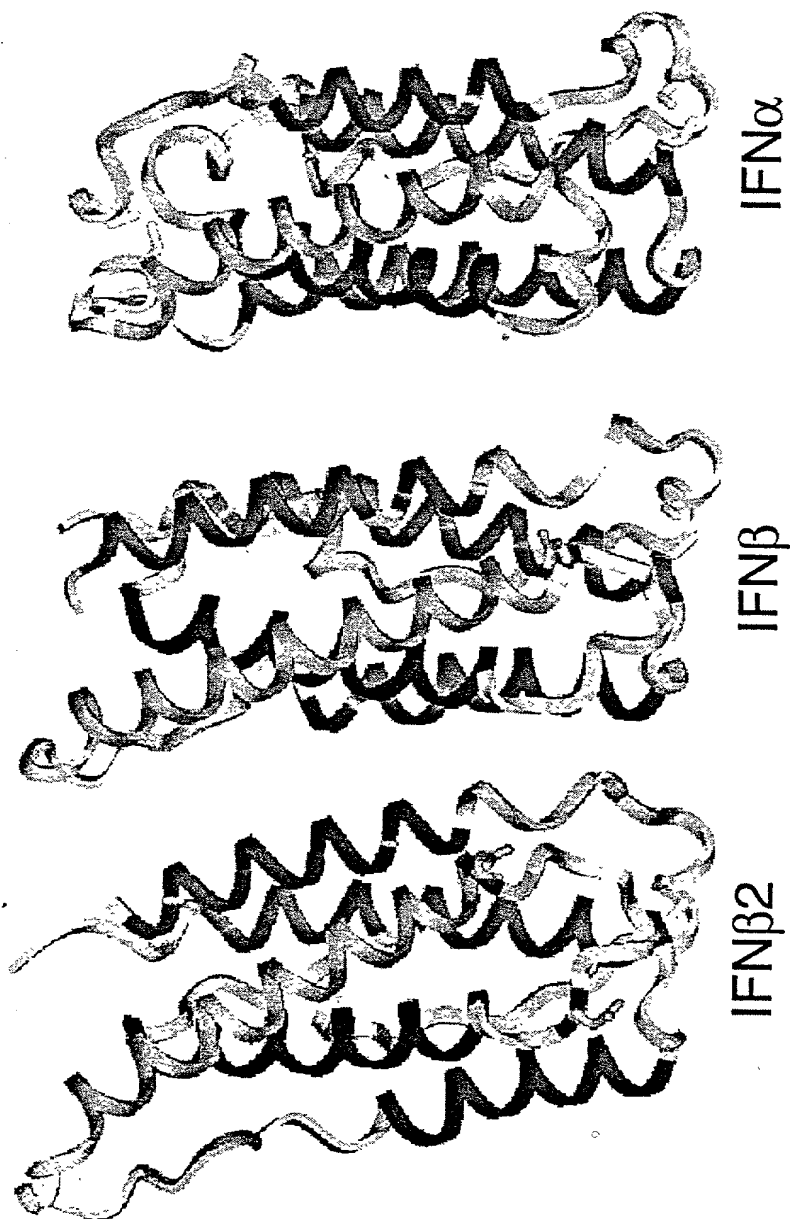


Figure 3

1 70

IFNB2 (1) MI~~IKHFFGT~~VLLAST~~IFSLDLKLI~~IFOOROVN~~QESLKL~~NKLIQ-TLSIQOCLPHRKNFLLPQKSLSP

IFNB (1) MTNKC~~LLQ~~TALL~~CFST~~HALSMSYNLLGFLQRSSNFQCQKLLWOLNGRLEY--CLKDRMNFDIPEEIKQL

IFNalpha8 (1) MALTFYLLVALVLSYKSFSSLGCDLPQTHS-LGNRRALILLAQMR-RISPFSCCLKDRHDFEFPQEEFDD

IFNalpha7 (1) MARSFSLLMVVLVLSYKSICSLGCDLPQTHS-LGNRRALILLAQMR-RISPFSCCLKDRHDFEFPQEEFDD

IFNalpha6 (1) MALPFALLMALVVLSCSSCSLDCDLPQTHS-LGHRRTMLLAQMR-RISLFSCLKDRHDFRFPQEEFDD

IFNalpha5 (1) MALPFVLLMALVVLNCKSICSLGCDLPQTHS-LGNRRALILLAQMR-RISPFSCCLKDRHDFRFPQEEFDD

IFNalpha4b (1) MALSFSLLMAVLVLSYKSICSLGCDLPQTHS-LGNRRALILLAQMR-RISHFSCCLKDRHDFGFPQEEFDD

IFNalpha21 (1) MALSFSLLMAVLVLSYKSICSLGCDLPQTHS-LGNRRALILLAQMR-RISPFSCCLKDRHDFGFPQEEFDD

IFNalpha2 (1) MALTFALLVALLVLSCKSSCSVGCGLPQTHS-LGSRRTMLLAQMR-RISLFSCLKDRHDFGFPQEEF-G

IFNalpha16 (1) MALSFSLLMAVLVLSYKSICSLGCDLPQTHS-LGNRRALILLAQMR-RISHFSCCLKDRYDFGFPQEEFDD

IFNalpha14 (1) MALPFALLMALVVLSCSSCSLGCNLSQTHS-LGNRRALILLAQMR-RISPFSCCLKDRHDFEFPQEEFDD

IFNalpha13 (1) MASPFALLMVLVLSCKSSCSLGCGLPETHS-LGNRRALILLAQMS-RISPFSCCLKDRHDFGFPQEEFDD

IFNalpha10 (1) MALSFSLLMAVLVLSYKSICSLGCDLPQTHS-LGNRRALILLGQMG-RISPFSCCLKDRHDFRFPQEEFDD

IFNomega1 (1) MALLFPLLAALVMTSYSPVGSGLGCDLPQNHG-LLSRNTLVLLHOMR-RISPFCLCKDRRDFRFPQEMVKG

IFNgamma (1) MKYT-SYLLA~~FO~~LCIVLGSGLGCYCODEYVKE---AENLK~~KYF~~NAG---H--SDVADNGTLE--LGILK

Consensus (1) MAL F LLMALLVLS KS CSLGCDLPQTHS L NRR L LLAQM RISPFSCCLKDRHDF FPQEEFDD

71 140

IFNB2 (70) QOYQKGHT~~LA~~LHEMLQOIFSLFRANISLDGWEENHTEKFLIOLHQOLEYLEALMGLAEKLSGTLGSDN

IFNB (69) QOFQKEDAA~~L~~TYEM~~Q~~IFAT~~FR~~ODSSSTGWN~~ET~~IVENLLANVYH~~Q~~INHLKTVLEEKTEKEDFTRGKLM

IFNalpha8 (69) QOFQKAQAISVLHEMIQQTFNLFSTKSSAALDETLLDEFYIELDQQLNDLESCVMQEVGVIESPLMYED

IFNalpha7 (69) HQFQKTQAISVLHEMIQQTFNLFSTEDSSAAWEQSLLEK~~F~~STELYQQLNDLEACVIOEVGVEETPLMNED

IFNalpha6 (69) NQFQKAE~~A~~ISVLHEVIQQTFNLFSTKSSV~~AW~~DERLLDKLYTELYQQLNDLEACVMQEVVWGGTPLMNED

IFNalpha5 (69) NQFQKAQAISVLHEMIQQTFNLFSTKSSATWDETLLDKFYTELYQQLNDLEACVMQEVGVETPLMNVD

IFNalpha4b (69) HQFQKTQAISVLHEMIQQTFNLFSTEDSSAAWEQSLLEK~~F~~STELYQQLNDLEACVIOEVGVEETPLMNVD

IFNalpha21 (69) NQFQKAQAISVLHEMIQQTFNLFSTKSSATWEQSLLEK~~F~~STELNQQQLNDMEACVIOEVGVEETPLMNVD

IFNalpha2 (68) NQFQKAETIPVLHEMIQQTFNLFSTKSSAAWDETLLDKFYTELYQQLNDLEACVIOGVGVTTETPLMKED

IFNalpha16 (69) NQFQKAQAISAFHEMIQQTFNLFSTKSSAAWDETLLDKFYIELFQQLNDLEACVTQEVGVEEIALMNED

IFNalpha14 (69) NQFQKAQAISVLHEMIQQTFNLFSTKNSSAAWDETLLDKFYIELFOQMN~~D~~LEACVIOEVGVEETPLMNED

IFNalpha13 (69) NQFQKAP~~A~~ISVLHELIQQTFNLFSTKSSAAWDEDLLDKFCTELYQQLNDLEACVMQEBERVGETPLMNAD

IFNalpha10 (69) NQFQKAQAISVLHEMIQQTFNLFSTEDSSAAWEQSLLEK~~F~~STELYQQLNDLEACVIOEVGVEETPLMNED

IFNomega1 (69) SQLOKAHVMSVLHEMLQOIFSLFHTERS~~SA~~AWNMTLLDQLHTGLHQOLQHLETCLLQVVGEGESAGA~~IS~~

IFNgamma (58) NWKEESDRKIMQSO~~LV~~SFYFKLFKNFKD---DOS-~~LO~~KSVETEKEDMN-VKFFNSNKKKR~~DD~~FEK~~ET~~NY

Consensus (71) NQFQKAQAISVLHEMIQQTFNLFSTKSSAAWDE LLDKF TELYQQLNDLEACV QEVGVEETPLMN D

141 210

IFNB2 (140) LRLQVKMYFRR~~I~~HDYLE-NQDYSTCAWA~~IV~~QVEISRCLFFVFSLTEKLSKQGRPLNDMKQELTTEFRSPR

IFNB (139) SSLH~~IK~~KRY~~Y~~GRILHYLK-AKEYSHCAWTIVRVEILRNFYFINRLTG~~Y~~LRN-----

IFNalpha8 (139) SILAVRKYFORITLYLT-EKKYSSCAWEVVRAEIMRSFSL~~S~~INLOKRLKSKE-----

IFNalpha7 (139) FILAVRKYFORITLYLM-EKKYSPCAWEVVRAEIMRSFSFSTNLKKGLRRKD-----

IFNalpha6 (139) SILAVRKYFORITLYLT-EKKYSPCAWEVVRAEIMRSFSSSRNLQERLRRKE-----

IFNalpha5 (139) SILTVRKYFORITLYLT-EKKYSPCAWEVVRAEIMRSFSLSANLQERLRRKE-----

IFNalpha4b (139) SILAVRKYFORITLYLT-EKKYSPCAWEVVRAEIMRSLSFSTNLQKRLRRKD-----

IFNalpha21 (139) SILAVK~~K~~YFORITLYLT-EKKYSPCAWEVVRAEIMRSFSLSKI~~F~~QERLRRKE-----

IFNalpha2 (138) SILAVRKYFORITLYLK-EKKYSPCAWEVVRAEIMRSFSLSTNLQESLRSKE-----

IFNalpha16 (139) SILAVRKYFORITLYLM-GKKYSPCAWEVVRAEIMRSFSFSTNLQKGLRRKD-----

IFNalpha14 (139) SILAVK~~K~~YFORITLYLM-EKKYSPCAWEVVRAEIMRSFSFSTNLQKRLRRKD-----

IFNalpha13 (139) SILAVK~~K~~YFRRITLYLT-EKKYSPCAWEVVRAEIMRSLSTNLQERLRRKE-----

IFNalpha10 (139) SILAVRKYFORITLYLI-ERKYSPCAWEVVRAEIMRSLSFSTNLQKRLRRKD-----

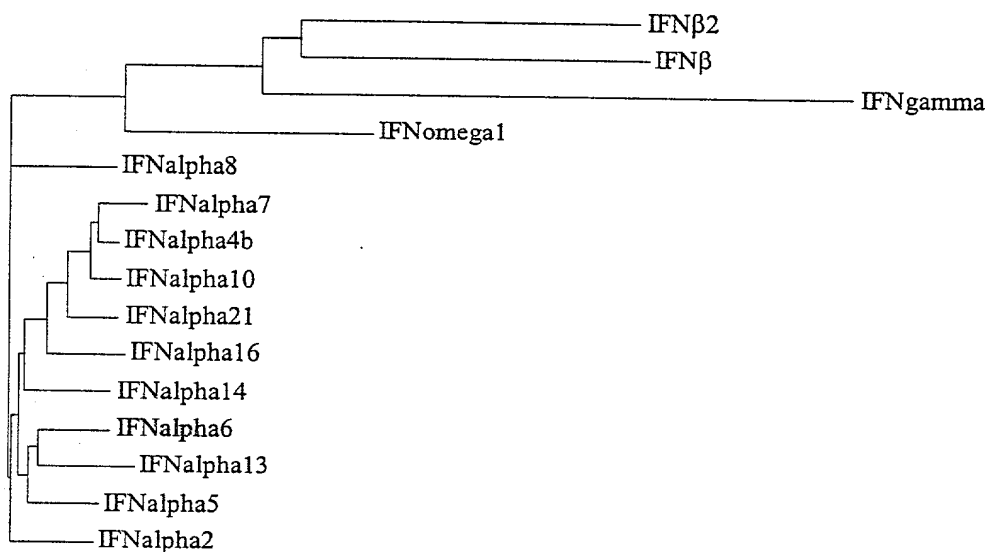
IFNomega1 (139) PALTLIRRYFQIRVY~~Y~~LK-EKKYSDCAWEVV~~R~~MEIMKSLFLSTNMQERLRSKORDLGSS-----

IFNgamma (122) SVTD~~L~~NVORKA~~I~~HEL~~I~~QVMAELSPA~~A~~KTGKR---KRSQML---FRGRRASQ-----

Consensus (141) SILAVRKYFORITLYL EKKYSPCAWEVVRAEIMRSFS STNLQ RLRRK

Figure 4

# Protein Level Comparison



# Nucleotide Level Comparison

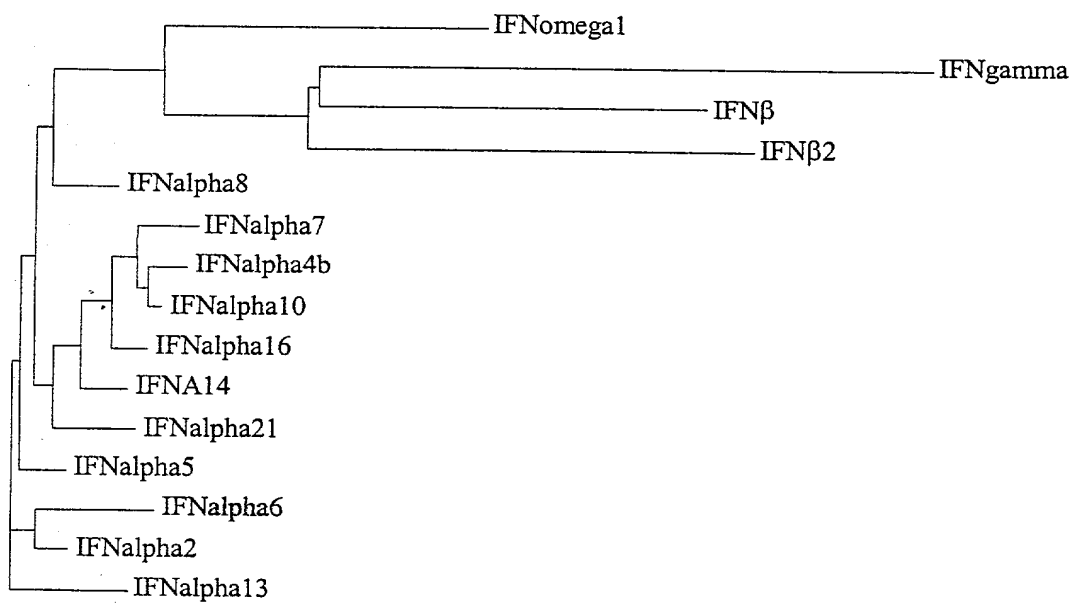


Figure 5

0901050 JFF

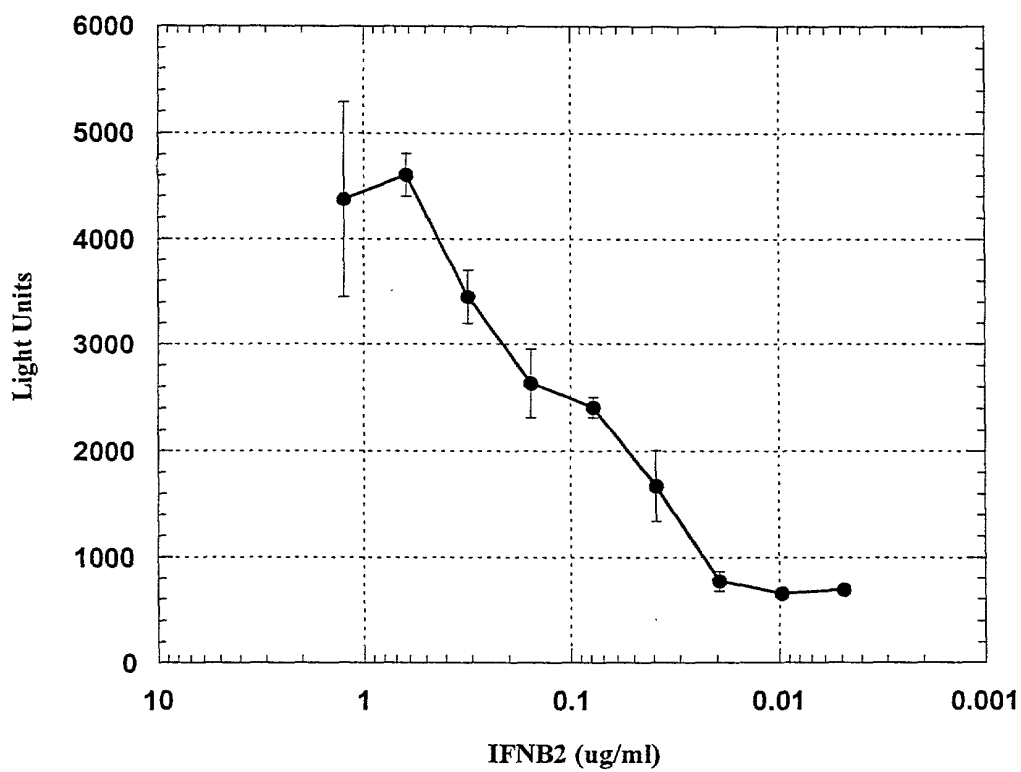


Figure 6

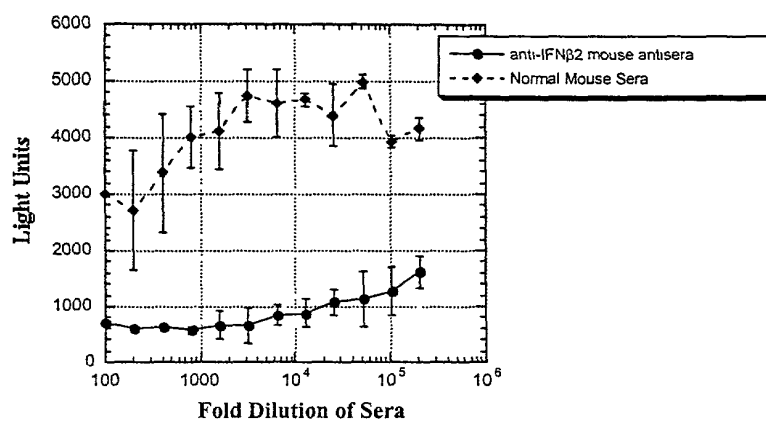
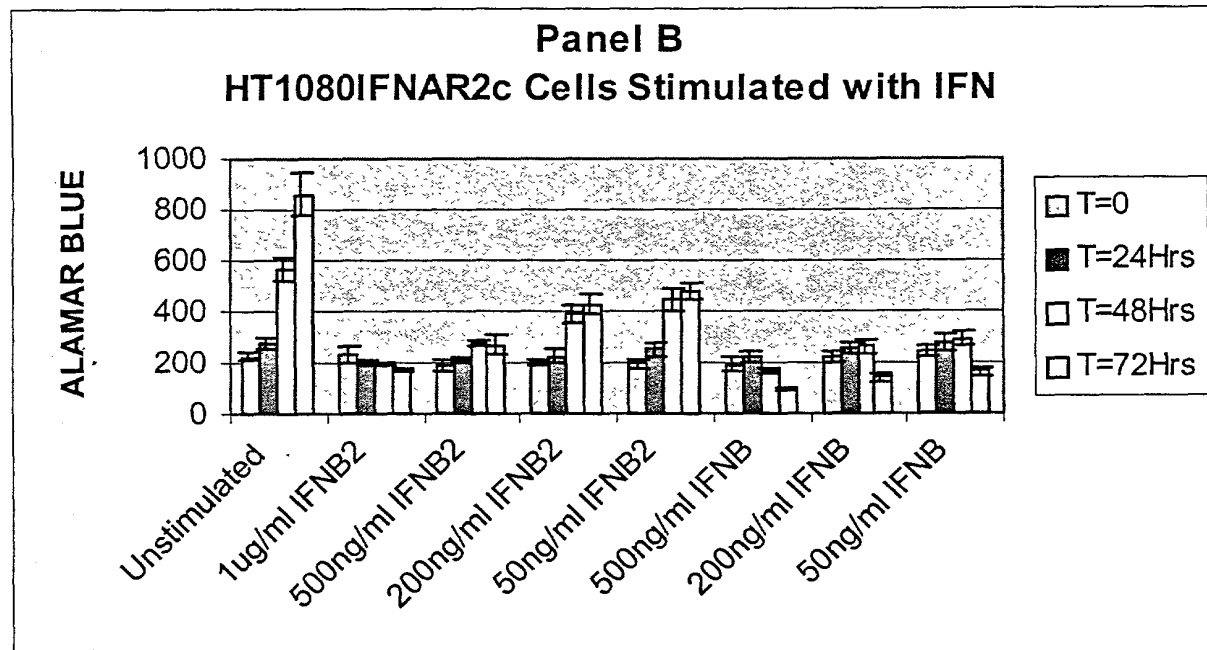
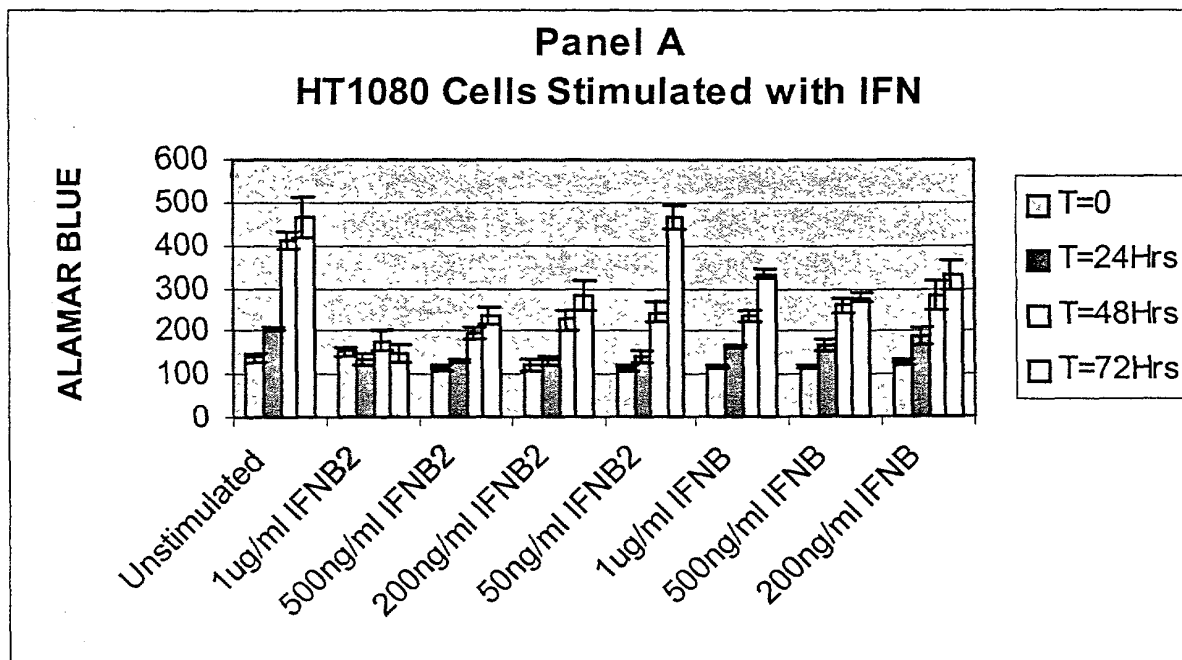


Figure 7



**Figure 8**



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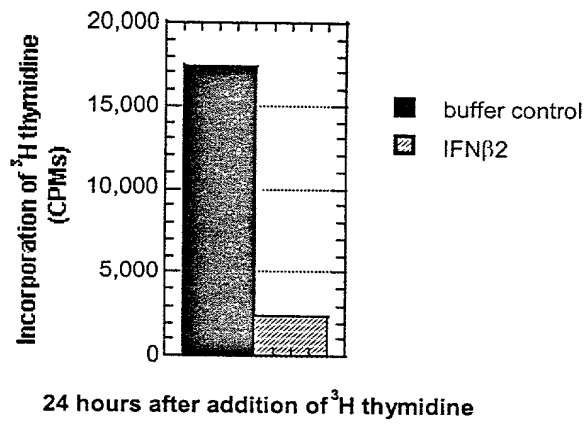


Figure 9

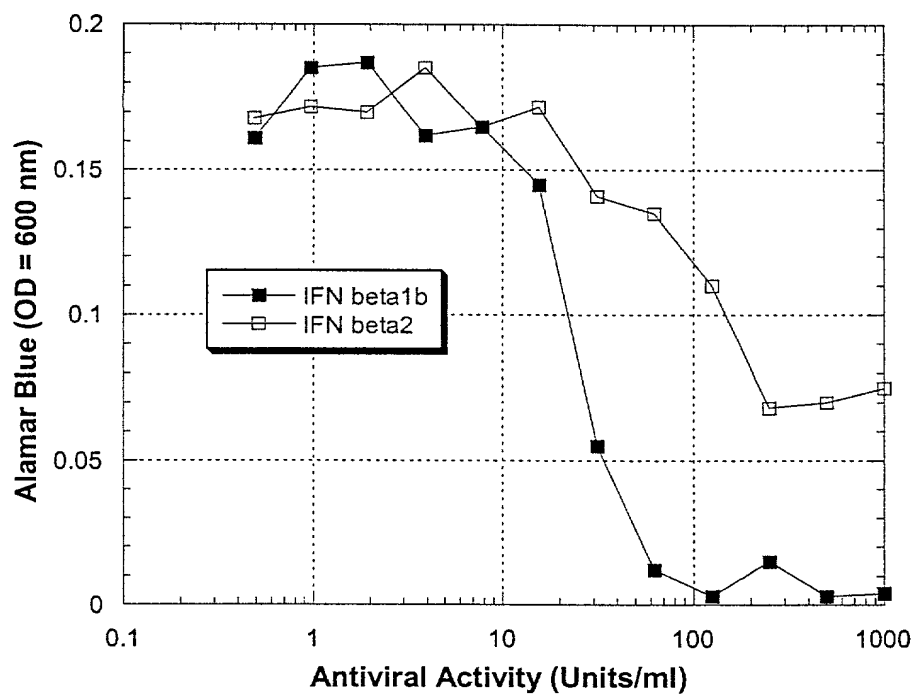


Figure 10

A bar chart with 'counts per minute' on the y-axis (0 to 3000) and two conditions on the x-axis: 'no competition' and '1000 fold cold'. The 'no competition' bar is approximately 2650 units high, and the '1000 fold cold' bar is approximately 150 units high.

Condition	Counts per minute
no competition	~2650
1000 fold cold	~150

**Figure 11**

1 tttaggtgac actatagaat actcaagctt gactaaatat ttagaaagca catttgtgttc  
61 agtgaaactt tgtatataat gaatagaata ataaaagatt atggttgatg actagtctgt  
121 aattgcctca aggaaagcat acaatgaata agttattttg gtacttcctc aaaatagcca  
181 acacaatagg gaaatggaga aaatgtactc tgaacaccat gaaaagggaa cctgaaaatc  
241 taatgtgtaa acttggagaa atgacattag aaaacgaaag ctacaaaaga gaacactctt  
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361 tatgcaggga taagtagcat atttgacctt cacc

Figure 12

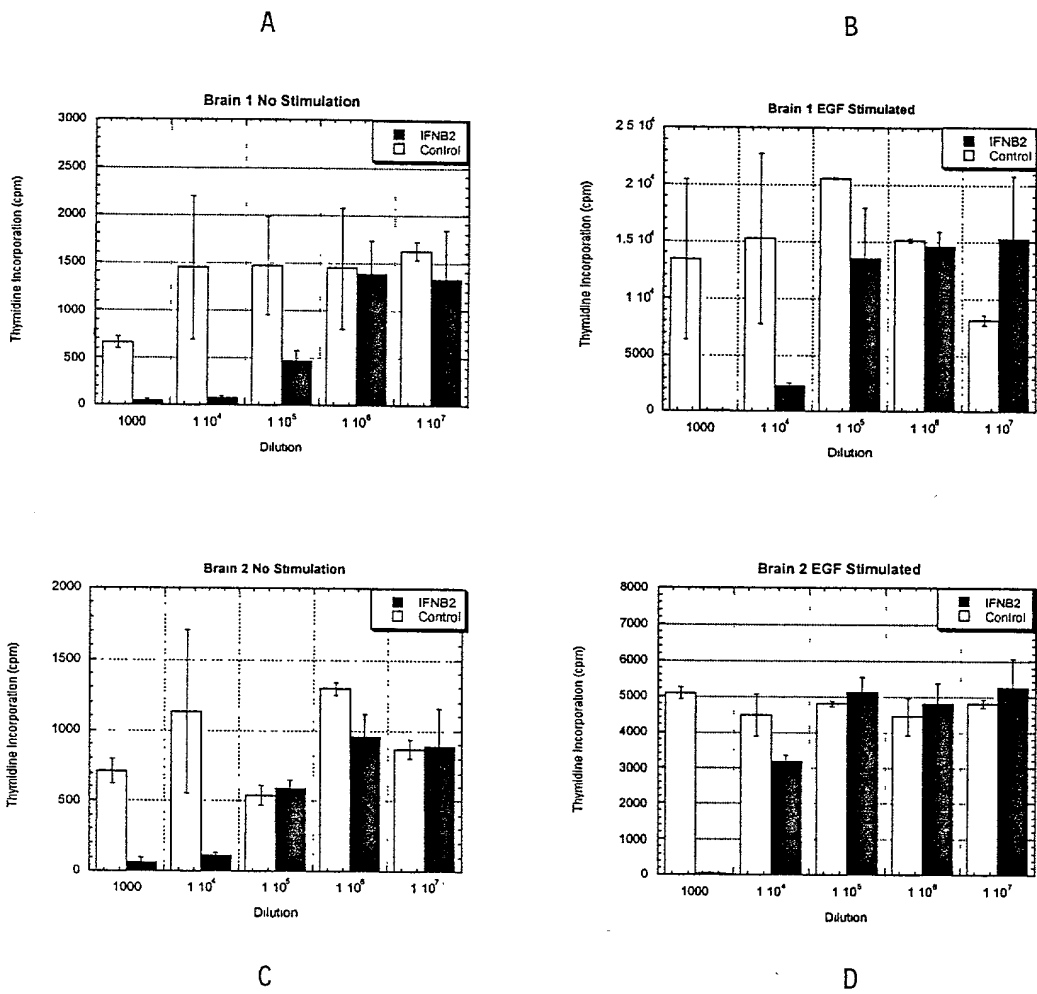
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481 ccagcaaaga caagtgaatc aagaaagttt aaaactcttg aataagttgc aaaccttgtc  
541 aattcagcag tgtctaccac acaggaaaaa ctttctgctt cctcagaagt ctttgagtcc  
601 ttaactgtac caaaaaggac acactctggc cattcttcat gagatgct

Figure 13

MIKHFFGTVLVLLASTTIFSLDLKLIIFQQRQVNQESLKLLNKLQTLISIQ  
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Figure 14

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"050T880"



**Figure 15**